



Db	379 ERCLVPSPK-VATYDQPEMSAAGYADKMIEQLEAGTHPFIMCNFAPPDMVGHGTGYEEA 437	Db	474 ----GVTLREGGR-LADVAPTMIDLLGVKKPAEMTGESLIQK 510
Qy	417 VKACOATDEAIGKIFEACOTNYVLMVTSDFHGNAEKMIAPDGSEHTAHTCNLYPTFCSKK 476	RESULT 3	
Db	438 VKACBTDIAIGRIVETOKHGYSLMTVADHGNAEKMKAAPDGKHTAHTCYRPLTISHP 497	C;Species: Listeria monocytogenes (strain EGD-AH1381	
Qy	477 TEVKSTPPGDDGKERABALRDYAPTVLQLMGLPVPPMDGVPLLEQ 524	C;Species: Listeria monocytogenes	
Db	498 GEKVE------DPADRHPLCDYAPTVLAIMGPAPAMTGSIVQK 538	C;Accession: AH1381	
RESULT 2			
AI1750	phosphoglycerate mutase homolog pgm [Imported] - Listeria innocua (strain Clip11262)	R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloch, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.	
C;Species: Listeria innocua	C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001	D.J. Jones, L.M.; Karst, U.	
C;Accession: AI1750	R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloche, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.	Science 294, 849-852, 2001	
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurpkat, G.; Madueño, E.; Maitournam, A.; Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Bernal, G.; Weh-ahok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Bernal, G.; Weh-ahok, C.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.	A;Title: Comparative genomics of Listeria species		
A;Reference number: AB1077; MUID:21537279; PMID:11679669	A;Accession: AH1381	A;Status: preliminary	
A;Molecule type: DNA	A;Gene: pgm	A;Nucleic acid type: DNA	
A;Residues: 1-510 <GLA>	C;Superfamily: phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent	A;Residues: 1-510 <GLA>	
A;Cross-references: GB:AL59202; PIDN: CAC97777.1; PID: g16415072; GSPDB: GN00178	A;Experimental source: strain Clip11262	A;Cross-references: GB:NC_003210; PIDN: CAD00534.1; PID: g16411944; GSPDB: GN00177	
A;Accession: AI1750	A;Gene: pgm	A;Experimental source: strain Clip11262	
A;Status: preliminary	C;Genetics:	A;Status: preliminary	
Query Match 41.0%; Score 1143.5%; DB 2; Length 510; Best Local Similarity 44.2%; Pred. No. 5.3e-84; Matches 230; Conservative 91; Mismatches 174; Indels 27; Gaps 7; C;Superfamily: phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent	Query Match 41.0%; Score 1143.5%; DB 2; Length 510; Best Local Similarity 44.0%; Pred. No. 7.7e-84; Matches 230; Conservative 92; Mismatches 174; Indels 27; Gaps 7; C;Superfamily: phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent	Query Match 41.0%; Score 1141.5%; DB 2; Length 510; Best Local Similarity 44.0%; Pred. No. 7.7e-84; Matches 230; Conservative 92; Mismatches 174; Indels 27; Gaps 7; C;Superfamily: phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent	
Db	6 VAIILDGFGKRAETVGVNAQANKPNFDRY - - - WADEFPHGIGKLAAGIDVGLPEGQGNK 61	Db	6 VAIILDGFGKRAETVGVNAQANKPNFDRY - - - WADEFPHGIGKLAAGIDVGLPEGQGNK 61
Qy	11 VCLVVIDGWGLSDEQHGNIAIAKAKTPIMDKLCGNWQ - - - KLEANGLHVGLPEGLGNK 65	Qy	11 VCLVVIDGWGLSDEQHGNIAIAKAKTPIMDKLCGNWQ - - - KLEANGLHVGLPEGLGNK 65
Db	6 VAIILDGFGKRAETVGVNAQANKPNFDRY - - - WADEFPHGIGKLAAGIDVGLPEGQGNK 61	Db	6 VAIILDGFGKRAETVGVNAQANKPNFDRY - - - WADEFPHGIGKLAAGIDVGLPEGQGNK 61
Qy	66 SEYGHLNIGAGRIVYQDITRINLAQVNRFETVNTPQIVASAERAKGSGRLHLIGLVSOGD 125	Qy	66 SEYGHLNIGAGRIVYQDITRINLAQVNRFETVNTPQIVASAERAKGSGRLHLIGLVSOGD 125
Db	62 SEYGHLNIGAGRIVYQDITRINLAQVNRFETVNTPQIVASAERAKGSGRLHLIGLVSOGD 125	Db	62 SEYGHLNIGAGRIVYQDITRINLAQVNRFETVNTPQIVASAERAKGSGRLHLIGLVSOGD 125
Qy	126 VHSHIDHPLALITRAFKQLOQPKVTFADGRDTSPGAGYEQQLLOFIASEKYGELAT 185	Qy	126 VHSHIDHPLALITRAFKQLOQPKVTFADGRDTSPGAGYEQQLLOFIASEKYGELAT 185
Db	122 VHSHINHLYVALLETAKDGKVKNYIHAFLGRVYAPQSSLEYETLQLKAISDNLYGAT 181	Db	122 VHSHINHLYVALLETAKDGKVKNYIHAFLGRVYAPQSSLEYETLQLKAISDNLYGAT 181
Qy	186 ITGRRYAMDRCRWERIKRIMAYEAIVGGIGQKATVDAIVVRRYQAQSETDEFIKPIVFS 245	Qy	186 ITGRRYAMDRCRWERIKRIMAYEAIVGGIGQKATVDAIVVRRYQAQSETDEFIKPIVFS 245
Db	182 VSRFYAMDRCRWERIKRIMAYEAIVGGIGQKATVDAIVVRRYQAQSETDEFIKPIVFS 245	Db	182 VSRFYAMDRCRWERIKRIMAYEAIVGGIGQKATVDAIVVRRYQAQSETDEFIKPIVFS 245
Qy	246 DDGR -- - VYKDDDTLIFENYRADMRQICECLGLERYKLDLNSVYPHPKNIQISGMQYNK 301	Qy	246 DDGR -- - VYKDDDTLIFENYRADMRQICECLGLERYKLDLNSVYPHPKNIQISGMQYNK 301
Db	240 KDGKPVATKDNDAVIFENRPRQIAQLSNAFTDKENDHFRADHPNPKFTVMTLYNP 299	Db	240 KDGKPVATKDNDAVIFENRPRQIAQLSNAFTDKENDHFRADHPNPKFTVMTLYNP 299
Qy	302 EFPFPLPPPTVITNLWLAQGQVTOFHCAKTEKPHVTFVNGGREGVQFDEDEROMV 361	Qy	302 EFPFPLPPPTVITNLWLAQGQVTOFHCAKTEKPHVTFVNGGREGVQFDEDEROMV 361
Db	300 SDAEVAEPIKVNICEVLSNEGLSQRRIATEKPHVTFMNGGRNEEFGENRLI 359	Db	300 SDAEVAEPIKVNICEVLSNEGLSQRRIATEKPHVTFMNGGRNEEFGENRLI 359
Qy	362 PSEPREVATDLPKPMNAAGVAAKMEVEQESGRPLVWNPAPPDMGHTGKPPPAVKACQ 421	Qy	362 PSEPREVATDLPKPMNAAGVAAKMEVEQESGRPLVWNPAPPDMGHTGKPPPAVKACQ 421
Db	360 NSPR-VETDLKPEMSAIEVTDALEVDIKNDKIDAIILNFANPMGHSQMLEPTIAKE 418	Db	360 NSPR-VETDLKPEMSAIEVTDALEVDIKNDKIDAIILNFANPMGHSQMLEPTIAKE 418
Qy	422 ATDEAIGKIFEACOTNYVLMVTSDFHGNAEKMIAPDGSEHTAHTCNLYPTCSSLKTVFK 481	RESULT 4	
Db	419 AVDENLGRVVDLLEKGSATIADHGNSETMTPPEGPHATAHTTVPVVTKK----- 473	T4865	
Qy	482 STPTGDDGKERABALRDYAPTVLQLMGLPVPPREMDCGVPLLEQ 524	C;Species: Bacillus stearothermophilus	
Db	474 ----GVTLREGGR-LADVAPTMIDLLGVKKPAEMTGESLIQK 510	C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 18-Aug-2000	



A;Cross-references: GB:299121; GB:AL009126; NID:92635827; PIDN:CA81596.1; PID:92635904	A;Experimental source: strain 168
A;Reference number: I40022; MUID:94292408; PMID:9460256; PIDN:AAA21680.1; PID:9460258	A;Accession: I40024
A;Status: preliminary; translated from GB/EMBL/IDB/J	A;Molecule type: DNA
A;Residues: 1-232; C <sup>+</sup> ; 234-431; 'MV'; 434-444; 'D'; 446-511 <RBS>	A;Cross-references: GB:L29475; NID:9460256; PIDN:AAA21680.1; PID:9460258
C;Keywords: intramolecular transferase; isomerase	C;Genetics:
A;Gene: pgm	C;Function:
A;Description: EC 5.4.2.1 [validated, MUID:94292408]	A;Note: 2,3-bisphosphoglycerate-independent but Mn <sup>2+</sup> -dependent enzyme [validated, MUID:94292408]
A;Superfamily: phosphoglycerate mutase; C <sub>2</sub> -bisphosphoglycerate-indpendent	C;Superfamily: intramolecular transferase; isomerase
Query Match 40.1%; Score 1118; DB 2; Length 511;	Best Local Similarity 42.7%; Pred. No. 6.1e-82; Mismatches 175; Indels 28; Gaps 6;
Matches 225; Conservative 99; Mismatches 175; Indels 28; Gaps 6;	
Qy 8 QQKQVCLVVDGWGLSDEOHGNAIAKAKTPIMDKVLCGSNW----OKLEAHGLHVGLPEGI_62	
Db 3 KKPAAILIDQFGGLRNETVGNAVALAKKPNFDRTI----WNOYPHOTLTASGEAGLPEEQ_58	
Qy 63 MGNSFEVGHNLNIGASRVIXQDIVRNLAVORNEFVTNPQIVASARAKKGSGRHLHLGYS_122	
Db 59 MGNSFEVGHNLNIGASRVIXQDIVRNLAVORNEFVTNPQIVASARAKKGSGRHLHLGYS_122	
Db 123 DGGVHSIDHFLAIFRAFKQLOQVKFVHFADGRDTSPTSPGAGYLEQOLQFQISEKYG_182	
Db 119 DGGVHSIDHFLAIFRAFKQLOQVKFVHFADGRDTSPTSPGAGYLEQOLQFQISEKYG_182	
Qy 183 LATITGTRYAMDRKRWERIKMAYEAIVYGIGQKATVDAVDVYVRYERAQSETDBFLKPI_242	
Db 179 IASISGRYIISMDRKWRWERIKMAYEAIVYGIGQKATVDAVDVYVRYERAQSETDBFLKPI_242	
Qy 243 FVSDP----GRVKKDDTLLFFNYRADMROIQCCEGLERYKDUNNSYPHPKNNQIISMT_297	
Db 237 VITKENGEPVAKIQDGSVLFYINRPRDIAQIISITFTNKFDRDGENYQPKNQYFVCT_296	
Qy 298 QYNKEFPFPLSFPPVHTNVLNLAQVTLASQGVTOFICAAETEKYPWTFEFFNGREYQFQDE_357	
Db 297 HFSEIVDGTVAFKRINLDNTVGEYLTSQHSLKQFLTAETEKYPWTFMSGGREAFPGRE_356	
Qy 358 RCMPSPSKPEVATYDLPKPPENAAQGAAYEKAQVIEQISGRPHLMCNAPPDMVGHGKFPAPV_417	
Db 357 RILINSPK-VATYDLPKPPENAAQGAAYEKAQVIEQISGRPHLMCNAPPDMVGHGKFPAPV_417	
Qy 418 KACQQTDEAIGKPIBACQTYNYVLMVTSQHNAERKMIAPDGSSEHTAHTCNLVPTCTSSKT_477	
Db 416 KAIEAVDECIGEVYDAILAKGGHAIITADHGNAQILITESGEPTAHHTNPVPIVTRG_475	
Qy 478 FVFKSTPPTGDDGKGERARALRDYAPTVLQLOMGLFPPPEMDGVPLLEQ_524	
Db 476 ITLR-----EGGLGDLAPTLDDLGyEKPKEGTGTSIQLQ_511	
RESULT 7	GB3004
C;Species: <i>Pseudomonas aeruginosa</i> (strain PA01)	C;Species: <i>Pseudomonas aeruginosa</i>
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000	C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: G83004	C;Accession: G83004
Qy 479 C;Reference number: A82950; MUID:20437337; PMID:10984043	C;Reference number: A82950; MUID:20437337; PMID:10984043

A; Status: preliminary	QY	39.1%	Score 1088.5;	DB 2;	Length 515;
A; Molecule type: DNA		Best Local Similarity 45.0%	Pred. No. 1-56-79;		
A; Residues: 1-151 <STO>		Matches 232;	Mismatches 180;	Indels 25;	Gaps
A; Cross-references: GB:AE004091; PIDN:99951424; PIDN:AG08516.1;					
A; Experimental source: strain PA01					
C; Genetics:					
A; Gene: Pgm; PA5131					
C; Superfamily: phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent					
Query Match	13	LWIDWGLSISDEQHNGNATAKAKTIPIMDKLICLGSQNWQL-EAHGHLVGLPREGMGNSEVGHL	7		
Best Local Similarity	10	LWIDLGFQHSESPDYNATAAKKPKPWDRLLATQPHGLISSGMDVGLPDQMGNSEVGHM	6		
Matches	232;	Conservative	78;	Mismatches	180;
Db					
QY	72	NIGAGRVTIDIVRINLAIVORNEFVTPNQIVASAERAKKGSGLRLHIGLVSDGGYHSHID	1		
Db	70	NLQAGRVVYQDFTRVTKAIRDGEFFENPYTAGYDVKAVADKAHVHLGLSPGGVHSHD	1		
QY	132	HFLALIRAFKQLQVPKVFLHEFAFGDRDTSPTSGAGLEQLLQFQASEKYGELATATGTRY	1		
Db	130	HLYVQAMQARRAGAKTIVLHAFJLGRDTTPKSAQPSLRLERDATPAQLGIGRASITGTRY	1		
QY	192	AMDDRKWRERIKKATVQDVKAVDVKVYDVRERYAQSSETDEFKLAPIVFSDDG	--	2	
Db	190	AMDDRNWRDRVQAAVYELIDGKAE-FTDASSVVALEAAVARGESDEFVATAVPPAGAEA	2		
QY	249	-RYKDDDTLJFENYRADMROIQCECLGLERYKDLNSYSPHKNIO1SG--MTQYNKEFP	3		
Db	249	VRVEDGDAF1FMNPRADRARELSRAFVEPAFNEF--BRERAQOLAGVQMLQIAAS1P	3		
QY	305	FPSLFPPVHTNNVLAEWLQASQNTQFHCAETEKYPHYTEFFENGREVOFQDERRCMVPPSP	3		
Db	305	ACPAFPPEPITVNVGLEYLAHKHQLQRLIAETEKYAHVTFPSGREGPEEGFEPERLIPSP	3		
QY	365	KEYATYDLPKEMNAAGVAEKMVIEQLESGRHPLVNCNFAPPDMWGTGKFPPVAKCQATD	4		
Db	365	K-WATYDLPQEMASPAEVTRIVEAIEQQRDYDVIVNYANGDMWGTGKFPEAAVRAVECLD	4		
QY	425	EAIGKJFEEACQTNYVILMVTSDHGNAAKM-TADPGSEHTAHTCNV1VPERCQSSKTFVEFKST	4		
Db	424	TCMGRIVEALDKYGEALITADHGNEQVMEDESTGQAHPTAHTCEPVPV----VYVGKRK	4		
QY	484	PPGDDGKERAARALDYAPTVLQVGLPVPPEMD	5.18		
Db	479	LSFREGG----VLAQDAPTMILUNGLEOPAEMNG	508		
RESULT 8					
G82335					
phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent					
C; Species: Vibrio cholerae					
C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001					
C; Accession: G82335					
R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; De					
charson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.					
I.; R.R. Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.					
Nature 406, 477-483, 2000					
A; Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cho					
A; Reference number: A82035; MUID:20406833; PMID:10952301					
A; Accession: G82335					
A; Status: preliminary					
A; Molecule type: DNA					
A; Residues: 1-510 <HEI>					
A; Cross-references: GB:AE004122; GB:AE003852; PIDN:9854745; PIDN:AAF93509.1;					
A; Experimental source: serogroup O1; strain N16961; biotype El Tor					
C; Genetics:					
A; Gene: VC0336					
A; Map position: 1					
C; Superfamily: phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent					

Query Match	38.9%	Score 1083.5;	DB 2;	Length 510;	Qy	68	VGHLNIGAGRIVYQDIVRINLAQVRNEFVTNQIVASAERAKKGSGRLHLGLVSDGGVH 127
Best Local Similarity	43.1%	Pred. No. 3.6e-79;				59	VGHVNIGAGRIVYQDLTRDVEIKEREFVLTNAVDQKNNAGKAVHLLGGLVSDGGVH 118
Matches 226;	Conservative 87;	Mismatches 180;	Indels 31;	Gaps 10;	Db		
Qy	6	NYQQKVLVQDGGWSLDEQHNGNAAKATPIMDKLCSGMQKL-BAHLGLVGLPGLMG 64			Qy	128	SHIDHHLFALIRAKFQKQGPVKVTFADGRDTSPTSGAGYLLQLOFTIASEKYGELAT 187
Db	2	SAKKPMALVILDGWGYREDNANNAINNARTPIMDSLMANPHTLISASGMGVGLPQMG 61			Db	119	SEDHIMAMVEAARGAEKIKLHAFLGDRDTPPSAEASLKEEDFKFAALGKGRASIV 178
Qy	65	NSEVGHLNIGAGRIVYQDIVRINLAYORNEFVTNQIVASAERAKKGSGRLHLGLVSDG 124			Qy	188	GRYYAMDRLKMERIKMAYEAIVGGIGOKATVDAVYVREYAOSETDEFLKPLVFSDD 247
Db	62	NSEVGHLNIGAGRIVDQFLTRTKAIDGEFOHNGKLVAAIDKAVAGKAIVHMGIMSPG 121			Db	179	GRYYAMDRLNRDRVAYDMLTLAQE-FQADTAVGLQAYARDNDEVKATVRAE 237
Qy	125	GYVHSIDHLFALIRAKFQKQGPVKVTFEADGRDTSPTSGAGYLEGQLQFIASEKYGELA 184			Qy	248	GR ---VKDDDTLIFFNKRADMROICECL---GLERYKDLNNSVPHPKNIQISGM 297
Db	122	GYVHSIDHLIYAAVEMAARGAEKIKYHCFDLDRDTPPSAEASLKFQDLEPKLGGRIA 181			Db	238	GQADAAMEGDGDLIEMNFRADARETRAFVNADFGFKRKYV-----NLNFVPL 289
Qy	185	TITGGRYAMDRDKRWERIKMAYEAIVGGIGOKATVDAVYVREYAOSETDEFLPIVF 244			Qy	298	QYNEKEFPPPSLPPPTVHTINVLAELWASQGVPTFHCAEDEKYHVTFFPENGGBEVQFQDEE 357
Db	182	STVGRYAMDRDNWDRVKEADLTLAAGQ-FTYDSAVEALQQAAREENDEFVYATEI 240			Db	290	EAADIKTAVAPPASLANTFGEWMAKNDKTCQLRISETEKYHVTFFPENGGEFPAGEE 349
Qy	245	SDGCR ---VKDDDTLIFFNKRADMROIC ---ECGLERYKDLNNSVPHPKNQISG 295			Qy	358	RCMVPSPSKVEATYDLKPEMNAQVAEKMVQEOLTESGRHPLVNGCFAPPDMVGHTKFPEAV 417
Db	241	RAAGQESAMQDDALIFMNTFADRAQIITRFPVDPAGFSR ---KAFFP ---AIDFVM 292			Db	350	RLLINSPK-VAYDLDQPEMSSAELTEKVAAESGKDTIICNPNMDMVGTGVMAAI 408
Qy	296	MTOYNYKFERPEPSLFFPPTHTNLAENLASOGYQTOFCAETEKYPHYTEFFNGREYQFQD 355			Qy	418	KACQATDEAIGKIFERACQTYNYLMTSDHGAEKMTAP-DGSEHTAHTCNLYPFTCSK 476
Db	233	LTOYADADPLQCAFQASLNTYGENSKAGTQLRISETEKYHVTFFPENGVNEFPG 352			Db	409	I:V:AEALONCIEQTCVYKAVSGK ---LSDIAPTMLSLGMETQEMTGKPL 503
Qy	356	EECMVPSKPEKATYDLKPEMNAQAGAEKMKVQEOLTESGRHPLVNCAPPDMVGHTKFPEV 415			Qy	477	TVFVKSTPPTGDDKERARALRDVAPTVQLQMLGPVPPMDGVPL 521
Db	353	EEFQLVASKP-VATYDLOPEMSSKELTDKLYVAIKSKYDATICNPNGDVAVHTSYEA 411			Db	464	IYGEKKNVAVSGK ---LSDIAPTMLSLGMETQEMTGKPL 503
Qy	416	AVKACQATDEAIGKIFERACQTYNYLMTSDHGAEKMTAP-GSEHTAHTCNLYPFTCS 474			RESULT 10		
Db	412	AVKACEAVDECIGRVAEIAKEVDQGLLNTADIGNAEMMIDPTGGHTAHTSLPVPL --- 468				AG2328	2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Imported] - <i>Nostoc</i> sp. (
Qy	475	SKTFVKSTPPTGDDKERARALRDVAPTVQLQMLGPVPPMDG 518				C;Species: <i>Nostoc</i> sp. PCC 7120	
Db	469	-IVGNGKAISLKEGGK ---LSDIAPTMALSDLDLDPADNSG 505				A;Note: <i>Nostoc</i> sp. strain PCC 7120 is a synonym of <i>Anabena</i> sp. strain PCC 7120	
						C;Date: 14-Dec-2001 #text-change 09-Dec-2002	
						C;Accession: AG2328	
						R;Kaneko, T.; Nakamura, Y.; Wolk, C. P.; Kuritz, T.; Sasaki, S.; Watanabe, A.; Iriku Nakazaki, N.; Shimpou, S.; Sugimoto, M.; Takazawa, M.; Yasuda, M.; Tabata DNA Res 8, 205-213, 2001	
						A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium <i>A</i> ;Reference number: AB1807; PMID:2155285; PMID:11759840	
						A;Accession: AG2328	
						A;Status: preliminary	
						A;Molecule type: DNA	
						A;Residues: 1-533 <KUR>	
						A;Cross-references: GB:BA000019; PIDN:BA75881.1; PID:917133317; GSPDB:GN00179	
						A;Experimental source: strain PCC 7120	
						C;Genetics:	
						A;Gene: 114182	
						C;Superfamily: phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent	
						Query Match Best Local Similarity 42.9%; Score 1078; DB 2; Length 533;	
						Matches 227; Conservative 85; Mismatches 179; Indels 38; Gaps 10;	
						Qy 11 VCLVLDGWGLSDEQHGNIAKAKARTPIMDKLQCGNWK---LEAHLHGVPEGLGMN 65	
						Db 9 WLVLDGWGYCEETRGNIAAKTPYMESL---WTAYPHLHTSGKAVLGPQGMN 64	
						Qy 66 SEYGHNLNIGAGRIVYQDIVRINLAQVRNEFVNQIVASAERAKKGSGRLHLGLVSDGG 125	
						Db 65 SEYGHNLNIGAGRIVPQELVRISPAVEDSILSNSALVKICQVRNRNGKHLVGLCSBGG 124	
						Db 126 VHSHIDHLFALIRAKFQKQGPVKVTFADGRDTSPTSGAGYLEQLQFIASEKYGELAT 185	
						Qy 125 VSHITHLFLGLDLAKEQRISEFCVIAHTDGRDTPGDNINASALDYINHVGIGRV 184	
	13	LVYDGGNGKLSDEQHNGNAAKATPIMDKLCSGMQKL-BAHLGLVGLPQMG 67			Db 186 ITGRYAMDRDKRWERIKMAYEAIV-GGIGQKATVDAVYVREYAOSETDEFLKPLV 244		
	3	LVLDGGYGYREEQDQDNLINAKTPVMDL---WAKRPHTLIDASLGLVPLDRQMGNE 58			Qy 186 ITGRYAMDRDKRWERIKMAYEAIV-GGIGQKATVDAVYVREYAOSETDEFLKPLV 244		

Qy	351	VQFODEERCPVPSKPEVATYDLKPEMNAQVAEKGTEISGRPLVMCNFAPPDMVGHT 410	Qy	351	VQFODEERCPVPSKPEVATYDLKPEMNAQVAEKGTEISGRPLVMCNFAPPDMVGHT 410
Db	351	EPFKGEDRLLNSPK-VATYDLQPEMSSAELTEKLVSAIGSGKDVIIICNYPNGDMVGHT 409	Db	351	EPFKGEDRLLNSPK-VATYDLQPEMSSAELTEKLVSAIGSGKDVIIICNYPNGDMVGHT 409
Qy	411	GKFPKAVAKCQDATEAIGKIFEAQCTNYVNLMTSDHGNAAEKM1AP-DGSEHTAHTCNLY 469	Qy	411	GKFPKAVAKCQDATEAIGKIFEAQCTNYVNLMTSDHGNAAEKM1AP-DGSEHTAHTCNLY 469
Db	410	GDFDAAVKAVETLDNCIEQVVAAYKAQDQLLTDHGNAEQMRDPAQHTAHTSPLV 469	Db	410	GDFDAAVKAVETLDNCIEQVVAAYKAQDQLLTDHGNAEQMRDPAQHTAHTSPLV 469
Qy	470	PFTCSSLK/FVFVFKSTPPGKPERARALDVAPIVQLQMLGPVPPMDGVPL 521	Qy	470	PFTCSSLK/FVFVFKSTPPGKPERARALDVAPIVQLQMLGPVPPMDGVPL 521
Db	470	PL----LYVGNNKAVKAVEGGK----LSDIAPMMSLMMEMETQEMTGSPL 511	Db	470	PL----LYVGNNKAVKAVEGGK----LSDIAPMMSLMMEMETQEMTGSPL 511
RESULT 12					
F96987		2,3-bisphosphoglycerate-independent phosphoglycerate mutase gene [Imported] - C1			
		C:Species: Clostridium acetobutylicum			
		C:Accession: F96987			
		C:Cross references: GB:AE001437; PIDN:AAK78689.1; PID:q15023592; GSPDB:GN00168			
		C:Sequence_revision: 14-Sep-2001 #text_change 30-Sep-2001			
		C:Experimental source: Clostridium acetobutylicum ATCC824			
		C:Genetics:			
		C:Gene: CAC0712			
		C:Superfamily: phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent			
		A:Reference number: A96900; MUID:21359325; PMID:21359325			
		A:Accession: F96987			
		A:Status: preliminary			
		A: Molecule type: DNA			
		A: Residues: 1-510 <KUR>			
		A:Cross references: GB:AE001437; PIDN:AAK78689.1; PID:q15023592; GSPDB:GN00168			
		A:Sequence_revision: 14-Sep-2001 #text_change 30-Sep-2001			
		C:Species: Clostridium acetobutylicum ATCC824			
		C:Accession: F96987			
		R; Holling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Daly, M.J.; Bennett, G.N.; Kooin, E.V.; Smith, D.R.			
		J. Bacteriol. 183, 4823-4838, 2001			
		A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium			
		A:Reference number: A96900; MUID:21359325; PMID:21359325			
		A:Accession: F96987			
		Query Match	38.2%	Score 1065; DB 2; Length 510;	
		Best Local Similarity	42.9%	Pred. No. 1.le-77; Gaps 10;	
		Matches 225; Conservative 99; Mismatches 176; Indels 24; Gaps 10;			
Qy	8	SEYGHNLIGAGRIVYQDIDIVRINLAVORNEFVTNQPIVASAERAKGSGRHLGLVSDGG 125	Qy	8	SEYGHNLIGAGRIVYQDIDIVRINLAVORNEFVTNQPIVASAERAKGSGRHLGLVSDGG 125
Db	62	SEYGHNLIGAGRIVYQSLKLTIKTAIEDGDEFKNAALKAVNNVLENDSTFLHMGLLSPGG 121	Db	62	SEYGHNLIGAGRIVYQDIDIVRINLAVORNEFVTNQPIVASAERAKGSGRHLGLVSDGG 125
Qy	126	VHSHIDHFLALIFRAFKQLOQPKVIFHFFADGRDTSPSCAGYLEQLQFIASERYGELAT 185	Qy	126	VHSHIDHFLALIFRAFKQLOQPKVIFHFFADGRDTSPSCAGYLEQLQFIASERYGELAT 185
Db	122	VHSHTNHKLGLQLAKKNNVKKVYFHAFLDGDPVSSAKEFIDYMEETGLGEIAT 181	Db	122	VHSHTNHKLGLQLAKKNNVKKVYFHAFLDGDPVSSAKEFIDYMEETGLGEIAT 181
Qy	186	ITGRYYAMDRDKWERKTRKMAVEATVGGIGQKAVTVKADDVREPYAQSTTDEFLKPIVFS 245	Qy	186	ITGRYYAMDRDKWERKTRKMAVEATVGGIGQKAVTVKADDVREPYAQSTTDEFLKPIVFS 245
Db	182	VSGRYYAMDNRNWRERELAYNAMVLGKGEA-ESAIKAVDASYHDNKTDEEVLPVTV 239	Db	182	VSGRYYAMDNRNWRERELAYNAMVLGKGEA-ESAIKAVDASYHDNKTDEEVLPVTV 239
Qy	246	DDGR--VKKDDDTLIFNNYRADMRQTCLEGLERYKDLNSSVYPPHPIINIQISSMTQYN 301	Qy	246	DDGR--VKKDDDTLIFNNYRADMRQTCLEGLERYKDLNSSVYPPHPIINIQISSMTQYN 301
Db	240	KECRPVATIKDKDSVIFNFRDQTRIAEAFDGFKRD--RNTIEFTMTYED 296	Db	240	KECRPVATIKDKDSVIFNFRDQTRIAEAFDGFKRD--RNTIEFTMTYED 296
Qy	302	EFPFSL FPPVHTHTNVLAEWLQSQTQFHCAETEKYPVHTPFFNGGREVQDFERCM 360	Qy	302	EFPFSL FPPVHTHTNVLAEWLQSQTQFHCAETEKYPVHTPFFNGGREVQDFERCM 360
Db	297	SFKGVDFAGPENITNTGEYVSNKGLNQRLTAETEYAHVTFENGQVEEPNKNEDRNL 356	Db	297	SFKGVDFAGPENITNTGEYVSNKGLNQRLTAETEYAHVTFENGQVEEPNKNEDRNL 356
Qy	361	VPSPKVATYD1KPEMNAQVAEKGTEISGRPLVMCNFAPPDMVGHTGKPERAKVAC 420	Qy	361	VPSPKVATYD1KPEMNAQVAEKGTEISGRPLVMCNFAPPDMVGHTGKPERAKVAC 420
Db	357	ISSPK-VATYDLKPEMSSAELTEKLVSAIGSGKDVIIICNYPNGDMVGHTGILEAAKKAV 415	Db	357	ISSPK-VATYDLKPEMSSAELTEKLVSAIGSGKDVIIICNYPNGDMVGHTGILEAAKKAV 415
Qy	421	QATDEAIGKIFEAQCTNYVNLMTSDHGNAAEKM1-APDGSEHTAHTCNLYVPTCSSLTFV 479	Qy	421	QATDEAIGKIFEAQCTNYVNLMTSDHGNAAEKM1-APDGSEHTAHTCNLYVPTCSSLTFV 479
Db	416	EVDECGLKIVDKVLDGSVFTADIGNESEQMDYNSNGKPMTAHTVVPVF----VYV 470	Db	416	EVDECGLKIVDKVLDGSVFTADIGNESEQMDYNSNGKPMTAHTVVPVF----VYV 470
Qy	480	FKSTPPTGDKGERARALDVAPIVQLQMLGPVPL 523	Qy	480	FKSTPPTGDKGERARALDVAPIVQLQMLGPVPL 523
Db	471	SNH----PAK1 NEGLADTPTM1DPM1IYDPEPDMCKSTP 510	Db	471	SNH----PAK1 NEGLADTPTM1DPM1IYDPEPDMCKSTP 510

RESULT 13	S47833	probable phosphoglycerate mutase (EC 5.4.2.1), 2,3-diphosphoglycerate-independent - Esch	B91190	hypothetical protein ECs4490 [imported] - Escherichia coli (strain 0157:H7, substrain
	N	Alternate names: hypothetical protein o514	C	hypothetical protein ECs4490 [imported]
	C	Species: Escherichia coli	C	Species: Escherichia coli
	C	Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 01-Mar-2002	C	Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
	C	Accession: S47833; F65161	C	Accession: B91190
	R;Plunkett, G.		R;Hayashi, T.; Makino, K.; Ohnishi, S.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.	
	A;Reference number: S47666	A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and g	DNA Res. 8, 11-22, 2001	
	A;Accession: S47833	A;Reference number: A99629; MUID:21156231; PMID:11258756	A;Reference number: 8	
	A;Status: preliminary	A;Accession: B91190	A;Accession: B91190	
	A;Molecule type: DNA	A;Molecule type: DNA	A;Molecule type: DNA	
	A;Residues: 1-514 <BLU>	A;Residues: 1-514 <BLU>	A;Residues: 1-514 <BLU>	
	A;Cross-references: EMBL:000019; PIDN:9466582; PIDN:181589.1; PIDN:9466750	A;Cross-references: GB:BA000007; PIDN:BA37913.1; PIDN:913363965; GSPDB:GN00154	A;Cross-references: GB:BA000007; PIDN:BA37913.1; PIDN:913363965; GSPDB:GN00154	
	R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Ferna, N.T.; Burland, V.; Riley, M.; Riley, M.; Riley, M.	A;Experimental source: strain 0157:H7, substrain RIMD 0509952	A;Experimental source: strain 0157:H7, substrain RIMD 0509952	
	A.; Rose, D.J.; Mau, B.; Shao, Y.	C;Genetics:	C;Genetics:	
	Science 277, 1453-1462, 1997	A;Gen: Ec4490	A;Gen: Ec4490	
	A;Title: The complete genome sequence of Escherichia coli K-12.	C;Superfamily: phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent	C;Superfamily: phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent	
	A;Reference number: A64720; MUID:97426617; PMID:3278503	A;Reference number: A64720; MUID:97426617; PMID:3278503	A;Reference number: A64720; MUID:97426617; PMID:3278503	
	A;Status: preliminary; nucleic acid sequence not shown; translation not shown	A;Status: preliminary; nucleic acid sequence not shown; translation not shown	A;Status: preliminary; nucleic acid sequence not shown; translation not shown	
	A;Cross-references: GB:AE000439; GB:U00096; NID:91790036; PIDN:AA76636.1; PIDN:91790041; PIDN:91790041	A;Cross-references: GB:AE000439; GB:U00096; NID:91790036; PIDN:AA76636.1; PIDN:91790041; PIDN:91790041	A;Cross-references: GB:AE000439; GB:U00096; NID:91790036; PIDN:AA76636.1; PIDN:91790041; PIDN:91790041	
	A;Accession: F65161	A;Accession: F65161	A;Accession: F65161	
	A;Experimental source: strain K-12, substrain MG1655	A;Experimental source: strain K-12, substrain MG1655	A;Experimental source: strain K-12, substrain MG1655	
	A;Cross-references: MG1655	A;Cross-references: MG1655	A;Cross-references: MG1655	
	A;Gene: ybo	A;Gene: ybo	A;Gene: ybo	
	C;Superfamily: phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent	C;Superfamily: phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent	C;Superfamily: phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent	
	C;Keywords: intramolecular transferase; isomerase	C;Keywords: intramolecular transferase; isomerase	C;Keywords: intramolecular transferase; isomerase	
	Query Match	Query Match	Query Match	Query Match
	Best Local Similarity 38.2%; Score 1063; DB 2; Length 514;	Best Local Similarity 38.0%; Score 1059; DB 2; Length 514;	Best Local Similarity 41.1%; Score 1059; DB 2; Length 514;	Best Local Similarity 41.1%; Score 1059; DB 2; Length 514;
	Matches 218; Conservative 99; Mismatches 173; Indels 40; Gaps 10;	Matches 218; Conservative 99; Mismatches 173; Indels 40; Gaps 10;	Matches 218; Conservative 99; Mismatches 173; Indels 40; Gaps 10;	Matches 218; Conservative 99; Mismatches 173; Indels 40; Gaps 10;
Qy	8 QOKVCLVVIDGWGLSDEQHGNIAIAKAKTPIMDKLCGNWQK ---LEAHLHVGLP EGL 62	5 KKP MVVYLTDGGYREEQDQNAIFSAKTPVNDAL ---WANRPHTLIDASCLEVGPDRQ 60	63 MGNSEVGHNLNTGAGRIVYDQIVRNIAVQRNEFVTPQIVASAERAKKGSGRLHLGLYS 122	61 MGNSEVGHNLNTGAGRIVYDQIVRNIAVQRNEFVTPQIVASAERAKKGSGRLHLGLYS 122
Db	5 KKP MVVYLTDGGYREEQDQNAIFSAKTPVNDAL ---WANRPHTLIDASCLEVGPDRQ 60	63 MGNSEVGHNLNTGAGRIVYDQIVRNIAVQRNEFVTPQIVASAERAKKGSGRLHLGLYS 122	61 MGNSEVGHNLNTGAGRIVYDQIVRNIAVQRNEFVTPQIVASAERAKKGSGRLHLGLYS 122	61 MGNSEVGHNLNTGAGRIVYDQIVRNIAVQRNEFVTPQIVASAERAKKGSGRLHLGLYS 122
Qy	63 MGNSEVGHNLNTGAGRIVYDQIVRNIAVQRNEFVTPQIVASAERAKKGSGRLHLGLYS 122	61 MGNSEVGHNLNTGAGRIVYDQIVRNIAVQRNEFVTPQIVASAERAKKGSGRLHLGLYS 122	61 MGNSEVGHNLNTGAGRIVYDQIVRNIAVQRNEFVTPQIVASAERAKKGSGRLHLGLYS 122	61 MGNSEVGHNLNTGAGRIVYDQIVRNIAVQRNEFVTPQIVASAERAKKGSGRLHLGLYS 122
Db	61 MGNSEVGHNLNTGAGRIVYDQIVRNIAVQRNEFVTPQIVASAERAKKGSGRLHLGLYS 122	61 MGNSEVGHNLNTGAGRIVYDQIVRNIAVQRNEFVTPQIVASAERAKKGSGRLHLGLYS 122	61 MGNSEVGHNLNTGAGRIVYDQIVRNIAVQRNEFVTPQIVASAERAKKGSGRLHLGLYS 122	61 MGNSEVGHNLNTGAGRIVYDQIVRNIAVQRNEFVTPQIVASAERAKKGSGRLHLGLYS 122
Qy	123 DCGVHSIDHFLALIFRAFKQLOQVKPFTHFADGRSTPSGGAGLEQLOLQFIASEKYGK 182	121 AGVGHSHEDHIMAVELAERGAEKYLHAFDGRTPRSAEStLKKFEERKFAAGLKGK 180	121 AGVGHSHEDHIMAVELAERGAEKYLHAFDGRTPRSAEStLKKFEERKFAAGLKGK 180	121 AGVGHSHEDHIMAVELAERGAEKYLHAFDGRTPRSAEStLKKFEERKFAAGLKGK 180
Db	121 AGVGHSHEDHIMAVELAERGAEKYLHAFDGRTPRSAEStLKKFEERKFAAGLKGK 180	121 AGVGHSHEDHIMAVELAERGAEKYLHAFDGRTPRSAEStLKKFEERKFAAGLKGK 180	121 AGVGHSHEDHIMAVELAERGAEKYLHAFDGRTPRSAEStLKKFEERKFAAGLKGK 180	121 AGVGHSHEDHIMAVELAERGAEKYLHAFDGRTPRSAEStLKKFEERKFAAGLKGK 180
Qy	183 LATITGRRYAMDRDKWERIKMAYEAIVGGIGQKATVDAVYVVRERYAQSETDEFLKPI 242	181 VASITGRRYAMDRDNWDRVEKAYDILTLAGE -FQADTAVGLQAYARDENDEFVKAT 239	183 LATITGRRYAMDRDKWERIKMAYEAIVGGIGQKATVDAVYVVRERYAQSETDEFLKPI 242	181 VASITGRRYAMDRDNWDRVEKAYDILTLAGE -FQADTAVGLQAYARDENDEFVKAT 239
Db	181 VASITGRRYAMDRDNWDRVEKAYDILTLAGE -FQADTAVGLQAYARDENDEFVKAT 239	183 LATITGRRYAMDRDKWERIKMAYEAIVGGIGQKATVDAVYVVRERYAQSETDEFLKPI 242	181 VASITGRRYAMDRDNWDRVEKAYDILTLAGE -FQADTAVGLQAYARDENDEFVKAT 239	181 VASITGRRYAMDRDNWDRVEKAYDILTLAGE -FQADTAVGLQAYARDENDEFVKAT 239
Qy	243 VFSDDGR ---VKDDDTLIFNYRADMRQICECL ---GLERVKDLNNSVPHFKNIQ 292	240 VIRAEGQPDAAMEDGQDGFNFRARARETRAFVNADFGFARKKV ---NVD 291	243 VFSDDGR ---VKDDDTLIFNYRADMRQICECL ---GLERVKDLNNSVPHFKNIQ 292	240 VIRAEGQPDAAMEDGQDGFNFRARARETRAFVNADFGFARKKV ---NVD 291
Db	240 VIRAEGQPDAAMEDGQDGFNFRARARETRAFVNADFGFARKKV ---NVD 291	243 VSGMTQNKKEFFPSLPPVHTNVAELAISQGTVQFHCACTEKKPHVTEFFNGREVQ 352	241 MEAAVKAVEALDHCVEEVAKAVESVCGQQLTADHGNAEQMRFPATGQAHFTNLNPVPL 470	240 VIRAEGQPDAAMEDGQDGFNFRARARETRAFVNADFGFARKKV ---NVD 291
Qy	241 MEAAVKAVEALDHCVEEVAKAVESVCGQQLTADHGNAEQMRFPATGQAHFTNLNPVPL 470	242 TCSKTFVFKSTPPTGDDGKEKARALRDVAPTVLQMLGVPVPEMDGVP 521	242 TCSKTFVFKSTPPTGDDGKEKARALRDVAPTVLQMLGVPVPEMDGVP 521	241 MEAAVKAVEALDHCVEEVAKAVESVCGQQLTADHGNAEQMRFPATGQAHFTNLNPVPL 470
Db	242 TCSKTFVFKSTPPTGDDGKEKARALRDVAPTVLQMLGVPVPEMDGVP 521	243 VSGMTQNKKEFFPSLPPVHTNVAELAISQGTVQFHCACTEKKPHVTEFFNGREVQ 352	243 VSGMTQNKKEFFPSLPPVHTNVAELAISQGTVQFHCACTEKKPHVTEFFNGREVQ 352	242 TCSKTFVFKSTPPTGDDGKEKARALRDVAPTVLQMLGVPVPEMDGVP 521
Qy	243 VSGMTQNKKEFFPSLPPVHTNVAELAISQGTVQFHCACTEKKPHVTEFFNGREVQ 352	244 FPEAVKACQATEAIGKIFEAQCTQYVNLMTSDHGNAEMKTP -DSEHTPAHTCMVLPF 471	244 FPEAVKACQATEAIGKIFEAQCTQYVNLMTSDHGNAEMKTP -DSEHTPAHTCMVLPF 471	243 VSGMTQNKKEFFPSLPPVHTNVAELAISQGTVQFHCACTEKKPHVTEFFNGREVQ 352
Db	244 FPEAVKACQATEAIGKIFEAQCTQYVNLMTSDHGNAEMKTP -DSEHTPAHTCMVLPF 471	245 VMLTEYAAKTVAYPAPSLVNTGEWMAKNDKTLQRISETEKVAHVTFNGGOVEES 351	245 VMLTEYAAKTVAYPAPSLVNTGEWMAKNDKTLQRISETEKVAHVTFNGGOVEES 351	244 FPEAVKACQATEAIGKIFEAQCTQYVNLMTSDHGNAEMKTP -DSEHTPAHTCMVLPF 471
Qy	245 VMLTEYAAKTVAYPAPSLVNTGEWMAKNDKTLQRISETEKVAHVTFNGGOVEES 351	246 FKEDRLLINSK -VATDQFEMSSAELTEKLVAAIKSGKRYDTIICNYPNGDMVGHGTV 410	246 FKEDRLLINSK -VATDQFEMSSAELTEKLVAAIKSGKRYDTIICNYPNGDMVGHGTV 410	245 VMLTEYAAKTVAYPAPSLVNTGEWMAKNDKTLQRISETEKVAHVTFNGGOVEES 351
Db	246 FKEDRLLINSK -VATDQFEMSSAELTEKLVAAIKSGKRYDTIICNYPNGDMVGHGTV 410	247 TCSKTFVFKSTPPTGDDGKEKARALRDVAPTVLQMLGVPVPEMDGVP 521	247 TCSKTFVFKSTPPTGDDGKEKARALRDVAPTVLQMLGVPVPEMDGVP 521	246 FKEDRLLINSK -VATDQFEMSSAELTEKLVAAIKSGKRYDTIICNYPNGDMVGHGTV 410
Qy	247 TCSKTFVFKSTPPTGDDGKEKARALRDVAPTVLQMLGVPVPEMDGVP 521	248 C86037	248 C86037	247 TCSKTFVFKSTPPTGDDGKEKARALRDVAPTVLQMLGVPVPEMDGVP 521
Db	248 C86037	249 FPEAVKACQATEAIGKIFEAQCTQYVNLMTSDHGNAEMKTP -DSEHTPAHTCMVLPF 470	249 FPEAVKACQATEAIGKIFEAQCTQYVNLMTSDHGNAEMKTP -DSEHTPAHTCMVLPF 470	248 C86037
Qy	249 FPEAVKACQATEAIGKIFEAQCTQYVNLMTSDHGNAEMKTP -DSEHTPAHTCMVLPF 470	250 Hypothetical protein ybo [imported] - Escherichia coli (strain 0157:H7, substrain ED	250 Hypothetical protein ybo [imported] - Escherichia coli (strain 0157:H7, substrain ED	249 FPEAVKACQATEAIGKIFEAQCTQYVNLMTSDHGNAEMKTP -DSEHTPAHTCMVLPF 470
Db	250 Hypothetical protein ybo [imported] - Escherichia coli (strain 0157:H7, substrain ED	C;Species: Escherichia coli	C;Species: Escherichia coli	250 Hypothetical protein ybo [imported] - Escherichia coli (strain 0157:H7, substrain ED
Qy	C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001	C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001	C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001	C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
Db	C;Accession: C86037	R;Perra, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May	R;Perra, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May	C;Accession: C86037
Qy	R;Grotbeck, B.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda	R;Grotbeck, B.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda	R;Grotbeck, B.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda	R;Grotbeck, B.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Db	471 ----IVGDKNVKAVAGGK ---LSDIAPTMSSLGMEIPQEMTGKPL 510	Nature 409, 529-533, 2001	Nature 409, 529-533, 2001	Nature 409, 529-533, 2001
Qy	471 ----IVGDKNVKAVAGGK ---LSDIAPTMSSLGMEIPQEMTGKPL 510	A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.	A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.	A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.

A; Reference number: A85480; MUID:21074935; PMID:11206551

A; Accession: C86037

A; Status: preliminary

A; Residues: 1-514 &lt;STO&gt;

A; Cross-references: GB:AE005174; NID:912518362; PIDN:AAG58759.1; GSPDB:GR00145; URGP:Z50

A; Experimental source: strain O157:H7, substrain EDL933

C; Genetics:

A; Gene: yibO

C; Superfamily: phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent

Query Match 38.0%; Score 1059; DB 2; Length 514;

Best Local Similarity 41.1%; Pred. No. 3.5e-77; Matches 218; Conservative 98; Mismatches 174; Indels 40; Gaps 10;

Qy 8	QQKVCLVVDGWLGSDEQHGNIAKAKTPTMDKLCGSGNQK-----LDAHGLVGLPQGSL 62
Db 5	KKPWLVLIDLGTYGTYREQQDNATSAKTPVMDA-----WANRPHTLIDASGLGVGLPDRQ 60
Qy 63	MGNSEVGHNLNIGAGRIVYQDIVRINLAQVNEFVTNPQVAVASERAKKGSGRHLGLVY 122
Db 61	MGNSEVGHNLNIGAGRIVYQDILTRDVLKDRRAFTNPVLTGAVDKAKNAGKAATHIMGLIS 120
Qy 123	DGGVHSIDHLFALTRAFKQLQVPKVIFHFDGDRDTSPSTSGAGYLEQOLQFIASEKYG 182
Db 121	AGGYVSHEDHIMANVLAERGAERKEKYLHAFLGRDTTPRSAESSLKKFEEKPAALGKGR 180
Qy 183	LATITGRYAMDRDKRWEIKMAYEAIVGIGORATVKAIVDVRERQAQSETDEFKRP 242
Db 181	VASTIGRYYAMDRONRWDRVEKADLTLIAQGF-QQADIAVAGIQAAVARDENDEFYRAT 239
Qy 243	VFSDDGR----VKDDDTLIFENYRADMRRQICECL-----GLERYKDLNNSVPHPKNIQ 292
Db 240	VIRAGEQPDAAAMEQDIALFMMFRADARAEITRAFVNADFDGPARKVY-----NVD 291
Qy 293	ISGMTOYKNEKFPPSLPPVTHNVLAEMLASGQVTPHCAEPEKPVTFNGNGREVQ 352
Db 292	FVMLTEYAADIKTAVAYPPASLYNTFGEMMAKNDKTQRLISETEKYAHVTFENGGEES 351
Qy 353	FQDBERKWPSPKEVATYDLKPEENAAQGAERKAEQITSGRHPVYMCNAPPDMVGITGK 412
Db 352	FKGEDRILNSPK-VATIDQOPENSAEETEKLVAASISGKYDTIICNPGDMVGHITGV 410
Qy 413	FEPAVKACOATDEAIGKIFEAACOTYYVLMVTSDFHGNAEKMTAP-DSSEHTAHTCNLVPF 471
Db 411	MEAAVKAVALDHCVEYAKAVESVGGQLLITADHGNAEQMRDPAQDAHTAHTNLPVPL 470
Qy 472	TCSSKTFYFKSTPPGDGKERAALRDVAPYTLQMLGLPVPPPEMDGYPL 521
Db 471	-----IYVGDKNYKAVAGCK-----LSDIAPTMUSLGMEMIPOEMTSRPL 510